

G. TURNER

1647

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/357,349

DATE: 11/21/2000  
TIME: 13:16:51

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Output Set: N:\CRF3\11212000\I357349.raw

3 <110> APPLICANT: Geerts, Hugo  
4 Masure, Stefan  
5 Cik, Miroslav  
6 Meert, Theo  
7 Ver Donk, Luc  
9 <120> TITLE OF INVENTION: Neurotrophic Growth Factor  
11 <130> FILE REFERENCE: 50936/702  
13 <140> CURRENT APPLICATION NUMBER: 09/357,349  
14 <141> CURRENT FILING DATE: 1999-07-14  
16 <150> PRIOR APPLICATION NUMBER: 9815283.8  
17 <151> PRIOR FILING DATE: 1998-07-14  
19 <150> PRIOR APPLICATION NUMBER: 09/248,772  
20 <151> PRIOR FILING DATE: 1999-02-12  
22 <150> PRIOR APPLICATION NUMBER: 09/327,668  
23 <151> PRIOR FILING DATE: 1999-06-08  
25 <160> NUMBER OF SEQ ID NOS: 15  
27 <170> SOFTWARE: PatentIn Ver. 2.0  
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30 <211> LENGTH: 339  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Homo sapiens  
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36 cagctcgtgc cggcgccgcg gctcggcctg ggcaccgct ccgacgagct ggtgcgtttc 120  
37 cgcttctgca cggcgtcctg ccgcccgcgc cgctctccac acgacctcag cctggccagc 180  
38 ctactgggcy ccggggccct gcgaccgcc ccgggctccc ggcctcag ccagccctgc 240  
39 tgccgaccca cgcgtacga agcggctctc ttcatggagc tcaacagcac ctggagaacc 300  
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50 ggggctgccg cctgcgctcg cagctgggag cggcgcgcgc gctcggcctg ggcaccgct 180  
51 ccgacgagct ggtgcgtttc cgcttctgca cgggctcctg ccgcccgcgc cgctctccac 240  
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53 ggcctcag ccagccctgc tgccgaccca cgcgtacga agcggctctc ttcatggagc 360  
54 tcaacagcac ctggagaacc ggggaccgcc tctccgccac cgctcgcgc tgccctgggc 420  
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58 <211> LENGTH: 113  
59 <212> TYPE: PRT  
60 <213> ORGANISM: Homo sapiens  
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63 Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys

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66 Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
67      20          25          30
69 Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
70      35          40          45
72 Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
73      50          55          60
75 Gly Ala Leu Arg Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
76      65          70          75          80
78 Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
79      85          90          95
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82      100          105          110
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97 Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly Ser
98      20          25          30
100 Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu
101      35          40          45
103 Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val
104      50          55          60
106 Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His
107      65          70          75          80
109 Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro
110      85          90          95
112 Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr
113      100          105          110
115 Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp
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123 <211> LENGTH: 819
124 <212> TYPE: DNA
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129 ccttccttga ggtccttcct ccccaagccc acctgggtgc cctctttctc cctgaggctc 120
130 cacttggtct ctccgcgcag cctgccttgt ggcccacctt ggccgctctg gctctgctga 180
131 gcagcgtcgc agagccctcc ctgggtctcg cgcctcgcag cctgcccccc cgcgaaggcc 240
132 cccgcctgt cctggcgtcc cccgcgggcc acctgcccgg taggtgagag ggcgaggggg 300
133 cggggcgggg ctggcccggg acaccgcgcg tgactgggtc tcattccagg gggacgcacg 360
134 gcccgctggg gcagtgaag agcccggcgg ccgcccgcgc ayccttctcg gcccgcgccc 420

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135 ccgcccgcctg caccceccatc tgcctctccc cgcgqgggccc gcgcgqgcgcg ggcctgggggc 480
136 ccgggcagcc gcgctcgggc agcgggggqcg cggggctgcc gccgcgcgc gcagctggg 540
137 ccggtcgcgc cgtcgcgcct gggccaccgc tccgacgagc tggcgcttt ccgctcttc 600
138 agcggctcct gcgcgcgcgc ccgctctcca caccacrtca gccgggccag cctactgggc 660
139 gcgggggccc tgcgaccacc cccgggctcc cggcccgta gccagccctg ctgccgacc 720
140 ccgcgcclacg aagcggctc cttcatggac gtcaacagca cctggagaac cgtggaccgc 780
141 ctctccgcca ccgctcgcg ctgcctgggc tgauggctc 819
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144 <211> LENGTH: 85
145 <212> TYPE: PRI
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148 <400> SEQUENCE: 6
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152 Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala Pro Leu
153 20 25 30
155 Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala
156 35 40 45
158 Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser
159 50 55 60
161 Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly
162 65 70 75 80
164 His Leu Pro Gly Arg
165 85
168 <210> SEQ ID NO: 7
169 <211> LENGTH: 159
170 <212> TYPE: PRT
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173 <400> SEQUENCE: 7
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175 1 5 10 15
177 Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro
178 20 25 30
180 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
181 35 40 45
183 Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
184 50 55 60
186 Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
187 65 70 75 80
189 Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala
190 85 90 95
192 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
193 100 105 110
195 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
196 115 120 125
198 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
199 130 135 140
201 Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
202 145 150 155

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212 utccccactc ccttgqcta qgcqgcaggt qagtgtttct cccagtact cctacctggt 120
213 actgaggaag ggcggcttga ctggtgaggg agagcagggc ttggcttggg cagcggttag 180
214 qtgtgggagq qaanaatggrc agggagggac caggtgaatg ggaggaggag cgggacttct 240
215 ctgaatggtr ggtgcaactca ggtgattcct cccctgggct cccagaggca gcaaacccat 300
216 tatactggaa cctaggccct tctgaqttt cccctccaca cagctaggag cccatgcccg 360
217 qactgatctc agccccagga cagccccctc ttgaggtcct tctcccccac gcccacctgg 420
218 gtqccctctt tctccctgag qctccacttg qtctctccgc gcagcctgcc ctgtggccca 480
219 ccttqccccc tctggtctct ctgagcagcg tcgcagaggg ctccctgggc tccqccccc 540
220 qcagccctgc ccccccgcaa gccccccgc ctgtcctggc glcccccgcc gcccacctgc 600
221 caggttaggtg agagggcgag qggqcggggc qggqctggcc cgggacaccy cgcgtgactg 660
222 ggtctcattc caqggggagc cacqggccgc tgggtcagtg gaagagcccg qcqcccgccg 720
223 ccgcagccct ctcggccccc gcccccgcgg cctgcacccc catctgctct tccccgcggg 780
224 ggcgcgcggg cgcgggctgg gggcccgggc agccgcgctc gggcagcggg ggcgcggggc 840
225 tgcgccttgc qctgcagctt ggtgcccgtg cgcgcgctcg qcctgggcca ccgctccgac 900
226 gagctggtgc gtttccgctt ctgcagcggc tectgcggcc gcgcgcgctc tccacacgac 960
227 ctcagccttg ccagcctact gggcgcgggg gccctgcgac gcccccggg ctccccggcc 1020
228 gtcagccagc cctgctgccc acccagcgcc tacgaagcgg tctccttcat ggacgtcaac 1080
229 agcaccttga gaaccgttga ccgctctctc gccaccgctt ggcgctgctt gggctgaggg 1140
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241 Pro Arg Arg Gln Ala Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp
242 20 25 30
244 Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser
245 35 40 45
247 Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro
248 50 55 60
250 Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg
251 65 70 75 80
253 Trp Cys Ser Gly Arg Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro
254 85 90 95
256 Ala Pro Pro Pro Pro Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg
257 100 105 110
259 Ala Ala Arg Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala
260 115 120 125
262 Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly
263 130 135 140
265 Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly

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266 145          150          155          160
268 Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu
269          165          170          175
271 Leu Gly Ala Gly Ala Leu Arg Pro Pro Gly Ser Arg Pro Val Ser
272          180          185          190
274 Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
275          195          200          205
277 Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys
278          210          215          220
280 Gly Cys Leu Gly
281 225
284 <210> SEQ ID NO: 10
285 <211> LENGTH: 220
286 <212> TYPE: PRI
287 <213> ORGANISM: Homo sapiens
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293 Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
294 20 25 30
296 Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
297 35 40 45
299 Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
300 50 55 60
302 Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
303 65 70 75 80
305 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro Pro
306 85 90 95
308 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
309 100 105 110
311 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
312 115 120 125
314 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
315 130 135 140
317 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
318 145 150 155 160
320 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
321 165 170 175
323 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
324 180 185 190
326 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
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335 <212> TYPE: DNA
336 <213> ORGANISM: Homo sapiens
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VERIFICATION SUMMARY  
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